Please amend the paragraph at page 7, lines 15-19 to read as follows:

--The primers used for the PCR amplification of the Hirt preparations were unsuitable for the analysis of genomic DNA preparations (low T_m). Therefore a new pair of primers, SEQ ID NO:3 and SEQ ID NO:4, respectively, was designed:

pBT338UP158, 5'-CCGGCTCGTATGTTGTGTGGAAT-3' (SEQ ID NO: 3) and

pBT338DO802, 5'-TGGCGAAAGGGGGATGTGCTG-3' (SEQ ID NO: 4).--.

Page 17, after line 31, please insert the attached Sequence Listing (2 pages).

In the Claims:

Please cancel claim 58.

Please amend claims 27, 28, 32, 33, 35-44, 49, 50, 52, 53, 55-57 and 59-60 to read as follows:

27. (Third Amendment) A method for mediating transgenic intramolecular recombination selected from deletions of DNA sequences located between two *six* sites and inversions of DNA sequences located between two *six* sites, in eukaryotic cells, comprising the step of transfecting eukaryotic cells with prokaryotic beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity;

wherein the prokaryotic beta recombinase is capable of using factors provided by the eukaryotic cells in order to mediate recombinase activity.

28. (Third Amendment) A method for mediating transgenic intramolecular recombination selected from deletions of DNA sequences located between two *six* sites and inversions of DNA sequences located between two *six* sites, in chromatin structures of

eukaryotic cells, comprising the step of transfecting eukaryotic cells with prokaryotic beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity;

wherein the prokaryotic beta recombinase is capable of using factors provided by the eukaryotic cells in order to mediate recombinase activity.

32. (Amended) A method according to claim 27, wherein an intramolecular recombination between two *six* sites in eukaryotic cells is obtained.

33. (Third Amendment) A method according to claim 32, wherein two or more intramolecular recombination events involving different DNA sequences located between different *six* sites occur at the same time.

35. (Amended) A method according to claim 32, wherein an intramolecular deletion of DNA sequences located between directly oriented *six* sites is obtained.

36. (Amended) A method according to claim 32, wherein an intramolecular inversion of DNA sequences located between inverted repeated *six* sites is obtained.

37. (Twice Amended) A method according to claim 32, wherein an intramolecular deletion of a DNA sequence located between two directly oriented *six* sites is obtained.

38. (Third Amendment) A method according to claim 32, wherein an intramolecular inversion of a DNA sequence located between two inversely oriented *six* sites is obtained.

39. (Third Amendment) A method according to claim 32, wherein an intramolecular deletion of a DNA sequence located between direct repeated DNA sequences containing *six* sites is obtained.

40. (Third Amendment) A method according to claim 32, wherein an intramolecular inversion of a DNA sequence located between inverted repeated DNA sequences containing *six* sites is obtained.

41. (Amended) A method according to claim 35, wherein the specific recognition sequence is located within an extrachromosomal DNA substrate.

42. (Amended) A method according to claim 36, wherein the specific recognition sequence is located within an extrachromosomal DNA substrate.

43. (Twice Amended) A method for catalyzing site-specific resolution of DNA sequences located between *six* sites in an extrachromosomal substrate transfected into an eukaryotic cell, comprising the step of catalyzing the site-specific resolution with beta recombinase; wherein the eukaryotic cell provides factors which beta recombinase is capable of using in order to mediate recombinase activity.

D5

44. (Amended) A method according to claim 43, wherein the extrachromosomal substrate is a plasmid.

49. (Twice Amended) A method according to claim 43, wherein the *six* sites are integrated into the genome of chromatin associated structures.

D6

Sub F4

50. (Twice Amended) A method according to claim 43, wherein the *six* sites are wrapped on a nucleosome at several locations.

52. (Third Amendment) A method according to claim 27, further comprising the steps of selecting mammalian cells from the group consisting of eukaryotic cells, transfecting the cells with prokaryotic beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity, and detecting the occurrence of an intramolecular recombination in the resulting transgenic mammalian cells.

D7

Sub E4

53. (Twice Amended) A method for mediating transgenic intramolecular recombination in eukaryotic cells, comprising the step of transfecting eukaryotic cells with prokaryotic beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity;

wherein the prokaryotic beta recombinase is capable of using factors provided by the eukaryotic cells in order to mediate recombinase activity; and

wherein the factors provided by the eukaryotic cells comprise HMG1 chromatin-associated protein.

55. (Twice Amended) A method for mediating transgenic intramolecular recombination in chromatin structures of eukaryotic cells, comprising the step of transfecting eukaryotic cells with prokaryotic beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity;

wherein the prokaryotic beta recombinase is capable of using factors provided by the eukaryotic cells in order to mediate recombinase activity; and

wherein the factors provided by the eukaryotic cells comprise HMG1 chromatin-associated protein.

56. (Amended) A method according to claim 28, wherein an intramolecular deletion of DNA sequences located between direct repeated *six* sites in the chromatin structures is obtained.

57. (Amended) A method according to claim 28, wherein an intramolecular inversion of DNA sequences located between inverted repeated *six* sites in the chromatin structures is obtained.

59. (Amended) A method according to claim 60, wherein the beta recombinase is a prokaryotic beta recombinase.

60. (Twice Amended) A method of mediating beta recombinase activity comprising the step of transfecting eukaryotic cells with beta recombinase and DNA sequences containing the natural *six* sites or modified versions that allow recombination activity; wherein the beta recombinase is capable of using eukaryotic cell factors of the eukaryotic cell to mediate recombinase activity.

Please add the following claims 61-63:

--61. (New) A method according to claim 60, wherein the eukaryotic cell factors comprise HMG1 chromatin-associated protein.--

--62. (New) A method according to claim 41, wherein the extrachromosomal DNA substrate is a plasmid.--

--63. (New) A method according to claim 42, wherein the extrachromosomal DNA substrate is a plasmid.--